



A curated Domain centric shared Docker registry linked to the Galaxy toolshed

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A curated Domain centric shared Docker registry linked to the Galaxy toolshed

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1 Genscale team -IRISA -Rennes, France

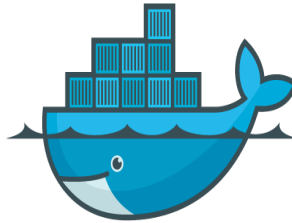
2 Genouest Bioinformatics facility – INRIA/IRISA – Rennes, France

3 French Institute of Bioinformatics – CNRS IFB-Core UMS3601 – Gif-sur-Yvette, France

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Docker : presentation



“**Docker** is an open-source engine to easily create **lightweight, portable, self-sufficient containers** from any application. The same container that a developer **builds** and **test** on a laptop can run at **scale**, in **production**, on Vms,[...], public **clouds** and more.”

Docker : presentation

Why using Docker containers to build, deploy and execute applications ?

- **Efficient** (no virtualization)
- **Isolation**
- **Build one time, execute “anywhere”**, independently of the execution platform (laptops, clusters and clouds with linux kernels)

...

Build : Dependencies & Dockerfile

```
FROM ubuntu:12.04
```

```
ADD . /script
```

```
ENTRYPOINT ["perl /script/analysis.pl"]
```

Run Docker

```
docker -run  
    containerUniqueID  
    -k=31 -i input.fastq -o output.bam
```

-The docker run command acts as a wrapper of the tool command line.

-Host directories (input, output,work...) can be mounted inside the container.

Google Container Engine

- A container based cloud architecture
- “With container-based computing, application developers can focus on their application code, instead of on deployments and integration into hosting environments”.

Docker on academic HPC clusters

- **Google Kubernetes** : an open source technology for containers life cycle management.
- **Docker Swarm** : allows to create and access to a pool of Docker hosts.
- **Genouest GO-DOCKER** : a batch scheduler like SGE, submitting jobs in Docker containers on top of Swarm..

Bioinformatics tools benchmarks with Docker

- cami-challenge.org : Critical Assessment of **Metagenomic** Interpretation
- <http://nucleotid.es> : continuous, objective and reproducible evaluation of genome **assemblers** using docker containers
- bioboxes.org : **interchangable** bioinformatics software containers

Galaxy Docker integration

- Docker can be used in Galaxy to :
 - manage tools dependencies : one tool , on Docker
 - Distribute populated Galaxy Distribution related to one topic

Shared registries : Docker Hub

- Not structured
- Not curated
- Not domain centric
- Not community driven

Shared registries : BIOSHADOCK

BIOSHADOCK

An initiative of the French Bioinformatics Institut
& the Genouest Bioinformatics Facility

Goals :

- Federate bioinformatics tools deployment procedures for the IFB cloud infrastructure
- Generate customized Galaxy cloud instances on the fly.
- Docker image indexation (service registry & searches)

Shared registries : BIOSHADOCK

BioShaDock registry

A **Bioinformatics Shared Docker** registry

 Browse BioShaDock

BioShaDock is a Bioinformatics Docker registry.

Here are hosted Docker images dedicated to a broad spectrum of Biological communities as represented by the [Biogenouest](#) Western France network.

In particular, you will find here :

- Command line tools ;

- Complexe web server frameworks.

- Galaxy Docker images that you can use with specific Docker Galaxy tools thanks to recent developments through the e-Biogenouest project (<https://www.e-biogenouest.org/>), (see [GUGGO](#) and our [Toolshed](#));


The number of images available will grow following the community needs.

The Docker GenOuest core facility team :

François Moreews, Cyril Monjeaud, Yvan Le Bras, Olivier Sallou



Shared registries : BIOSHADOCK



BioShaDock

Home / Images


Images

Search for an image

Images (34/34):

- abyss
- bio-linux
- biojava
- bioperl
- biopython
- blast
- bowtie
- bwa
- centos
- centos7
- chado_database
- clustal-omega
- comet
- discosnp
- emboss
- idba
- ipython-notebook
- megahit
- minia

docker-ui.genouest.org/#/tag/library/stacks_galaxy/latest/5f778585c808b968fe865159eda886a48f5e1bf82



BioShaDock

Home / Images / stacks_galaxy / latest

Details for tag library / stacks_galaxy : latest

want to use this image ?

#pull command :

```
docker pull docker-registry.genouest.org/stacks_galaxy:latest
```

#run test command:

```
docker run -i -t docker-registry.genouest.org/stacks_galaxy:latest /bin/bash
```

remark: if the docker client generates an ssl certificate error you can solve this issue adding on option "--insecure-registry docker-registry.genouest.org" in the docker daemon command line. modify the docker daemon command line adding the following option :
DOCKER_OPTS="--insecure-registry docker-registry.genouest.org" the docker daemon command should be something like "docker -d --insecure-registry docker-registry.genouest.org"
To do this on Ubuntu, modify /etc/init/docker.conf, on Debian , modify /etc/init.d/docker. Do not forget to restart the service : (service docker restart)

Image Details

General information [Image Ancestry](#)

Author

Comment

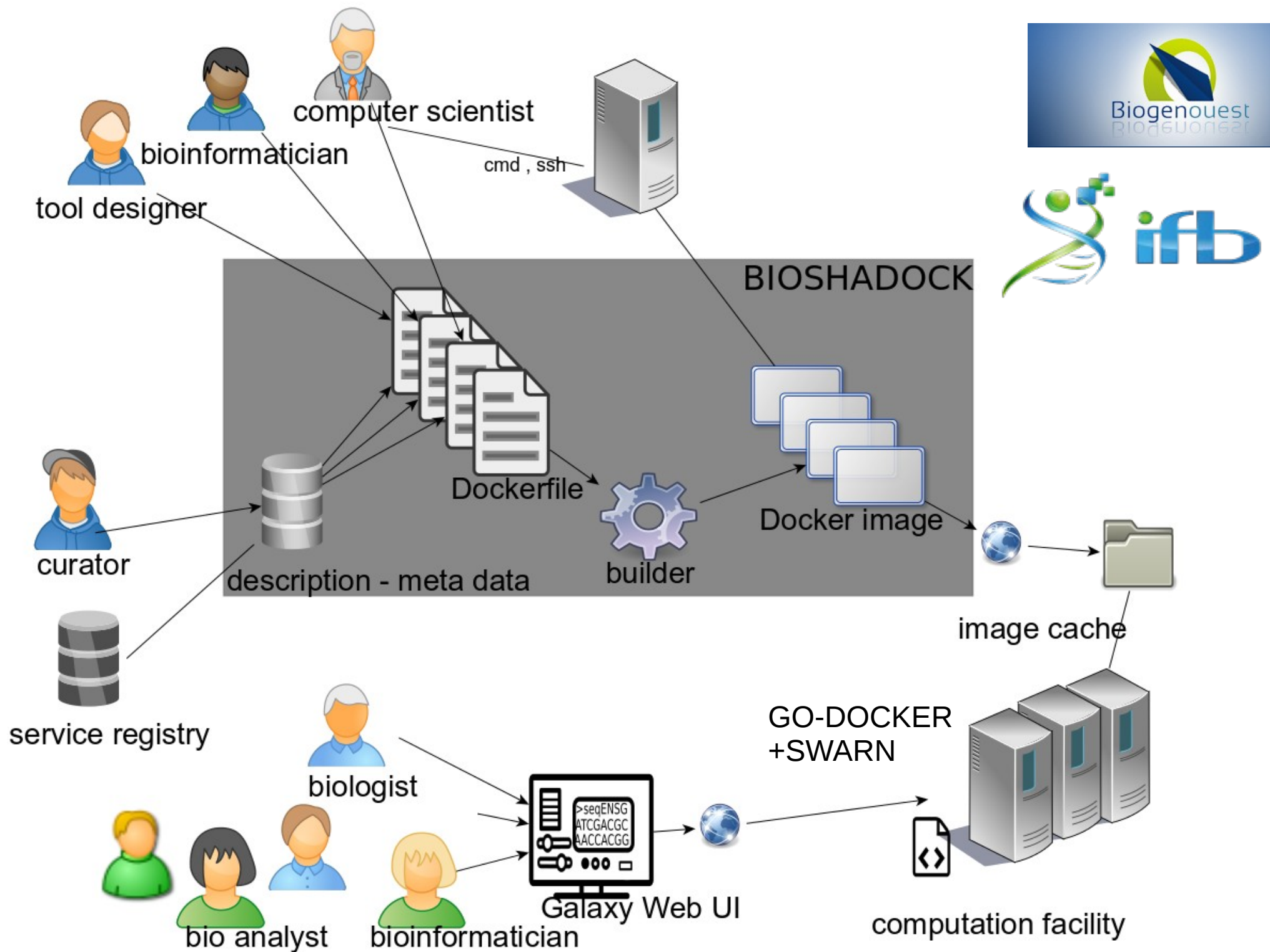
add STACKS .py wrappers for Galaxy on /usr/bin/

Created 18 days ago (2014-11-07 10:45:19 +0100)


Docker version 1.3.0

Shared registries : BIOSHADOCK

- BIOSHADOCK
 - Focuses on the model “on tool, one docker image”
 - Allows Dockerfile build
 - Manages permissions (private/ public images)
 - May integrate meta data to facilitate query and service registry searches
 - One unique repository for softwares with or without tool.xml => SAAS + CMD
 - Integrated to Galaxy by redefining tools dependencies in a Toolshed



BIOSHADOCK TOOLSHED integration

 **Galaxy Tool Shed**

Repositories Help User

164 valid tools on Jul 06, 2015

Search

- Search for valid tools
- Search for workflows

Valid Galaxy Utilities

- Tools
- Custom datatypes
- Repository dependency definitions
- Tool dependency definitions

All Repositories

- Browse by category

Available Actions

- Login to create a repository

toolshed.genouest.org

Repositories by Category

| Name | Description |
|--|--|
| Alignment | Alignment tools |
| Data management | Tools for data management |
| Data manager | Biological data management |
| Data source | data source |
| Fasta / Fastq manipulation | Fasta / Fastq manipulation |
| France Genomique Assembly | Tools for NGS assembly as part of France Genomique Project |
| Metadata management | Tools for ISA manipulation |
| Metagenomics | NGS metagenomics analysis tools |
| Microarray | Analyse gene expression data through microarray technology |
| Next Generation Sequencing | NGS analysis tools |
| Phylogeny | phylogeny tools |

BIOSHADOCK cluster /cloud integration using GO-DOCKER

Go-Docker

[Home](#)

[Resources](#)

[Login](#)

Go-Docker

0

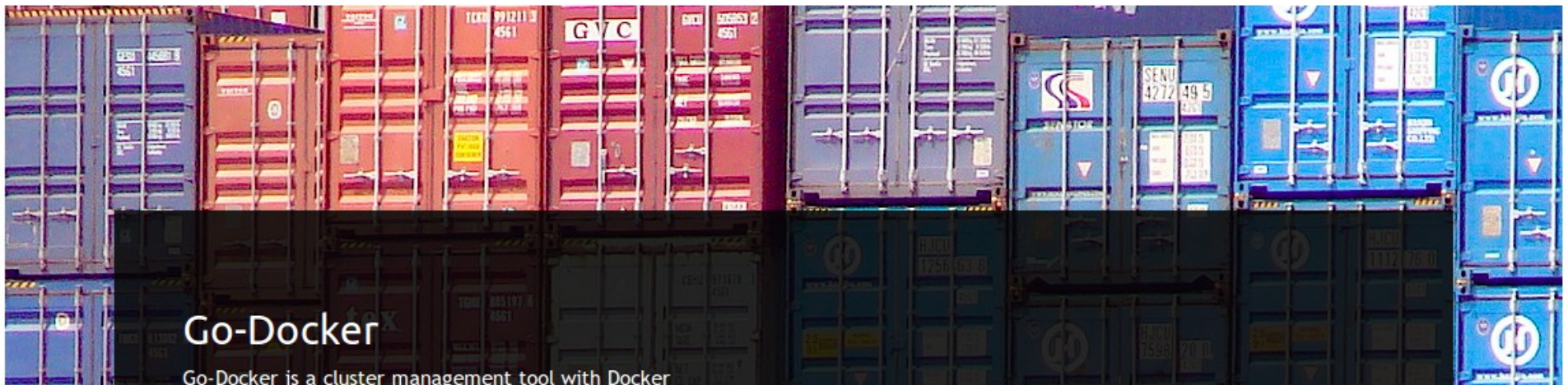
Containers pending

0

Containers running

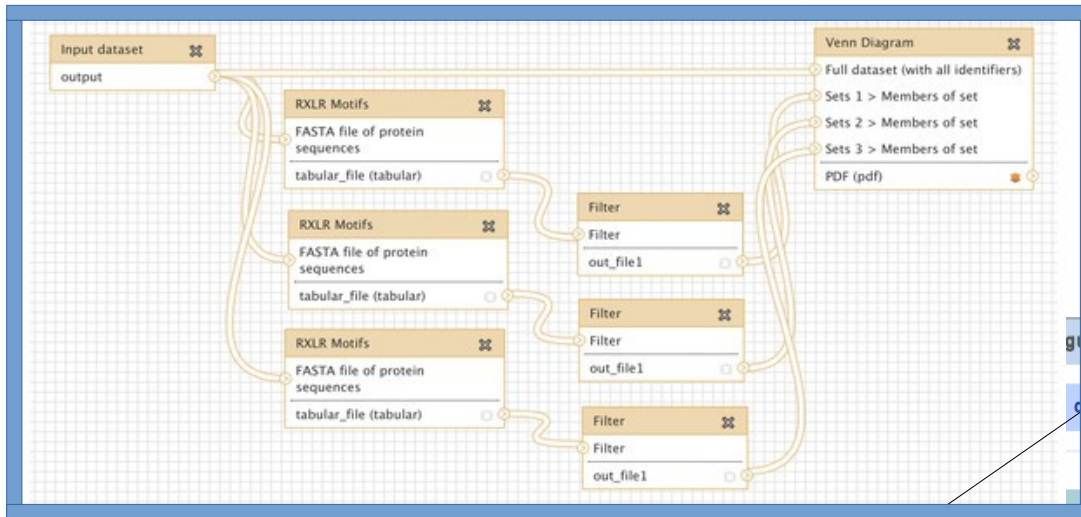
164

Containers to date



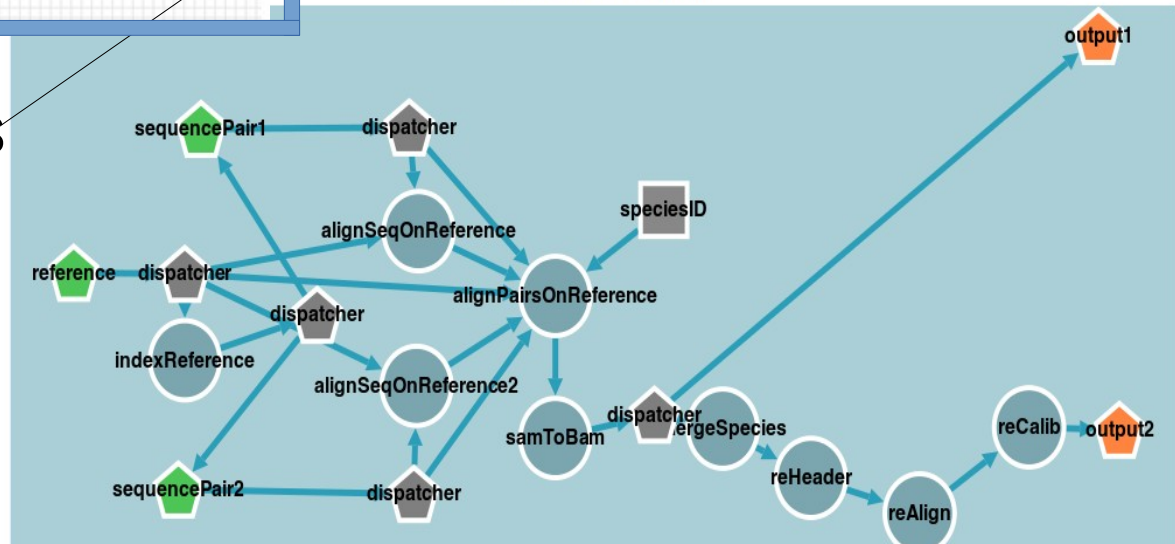
Build it one time, use it as you want

Command lines



A screenshot of a terminal window showing a table of job status. The table has columns: Job-ID, Prior, Name, User, State, Submit/Start, and CPUs. The table lists several jobs, including 'Sleeper1', 'Sleeper2', 'F12', 'F14', and 'F14'. The jobs are in various states, including 'deadline' and 'qu'. The table also shows a summary of jobs and a list of hosts with their CPU, Load, Memory, and Swap usage.

Galaxy tools & workflows



BIOSHADOCK

Other SAAS tools

References

- Genouest GO-DOCKER : <http://www.genouest.org/?p=246>
- Google Kubernetes, Docker container cluster management : kubernetes.io
- BioShaDock, a Bioinformatics Shared Docker registry : <http://docker-ui.genouest.org>
- GUGGO Galaxy Tooshed : <http://toolshed.genouest.org>
- Nucleotid.es, continuous, objective and reproducible evaluation of genome assemblers using docker containers : <http://nucleotid.es>
- ELIXIR Tools and Data Services Registry : <https://elixir-registry.cbs.dtu.dk>
- Bioboxes, a standard for creating interchangeable bioinformatics software containers : <http://bioboxes.org>
- IFB academic Cloud : <http://www.france-bioinformatique.fr/?q=en/core/e-infrastructure-team/ifb-cloud>